

L. Helms

#10

1642

RAW SEQUENCE LISTING      DATE: 07/06/2000  
 PATENT APPLICATION: US/09/203,768A      TIME: 13:01:24

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3 <110> APPLICANT: Huse, William D.  
 4     Watkins, Jeffrey D.  
 6 <120> TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods  
 7     of Use  
 9 <130> FILE REFERENCE: P-IX 2947  
 11 <140> CURRENT APPLICATION NUMBER: 09/203,768A  
 12 <141> CURRENT FILING DATE: 1998-12-02  
 14 <160> NUMBER OF SEQ ID NOS: 8  
 16 <170> SOFTWARE: PatentIn Ver. 2.0  
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 21 <213> ORGANISM: Homo sapiens  
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 25 <222> LOCATION: (1)..(417)  
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 28 <221> NAME/KEY: sig\_peptide  
 29 <222> LOCATION: (1)..(57)  
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 36 gtc ctg tcc cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag     96  
 37 Val Leu Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys  
 38                     20                     25                     30  
 40 cct tcg gag acc ctg tcc ctc acc tgc gct gtc tat ggt ggg tcc ttc     144  
 41 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe  
 42                     35                     40                     45  
 44 agt ggt tac tac tgg agc tgg atc cgc cag ccc cca ggg aag ggg ctg     192  
 45 Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu  
 46     50                     55                     60  
 48 gag tgg att ggg gaa atc aat cat agt gga agc acc aac tac aac ccg     240  
 49 Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro  
 50     65                     70                     75                     80  
 52 tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc aag aac cag     288  
 53 Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln  
 54                     85                     90                     95  
 56 ttc tcc ctg aag ctg agc tct gtg acc gcc gcg gac acg gct gtg tat     336  
 57 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr  
 58                     100                     105                     110  
 60 tac tgt gcg aga gaa ata gca gct cgt cct cac cga tac ttt gac tac     384  
 61 Tyr Cys Ala Arg Glu Ile Ala Ala Arg Pro His Arg Tyr Phe Asp Tyr  
 62                     115                     120                     125  
 64 tgg ggc cag gga acc ctg gtc acc gtc tcc tca     417  
 65 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 66     130                     135

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79           20           25           30
81 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
82           35           40           45
84 Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
85           50           55           60
87 Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro
88   65           70           75           80
90 Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
91           85           90           95
93 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
94           100          105          110
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119   1           5           10           15
121 gcc acc ctg tct gtg tct cca ggg gaa aga gcc acc ctc tcc tgc agg 96
122 Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
123           20           25           30
125 gcc agt cag agt gtt agc agc aac tta gcc tgg tac cag cag aaa cct 144
126 Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro
127           35           40           45
129 ggc cag gct ccc agg ctc ctc atc tat ggt gca tcc acc agg gcc act 192
130 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
131           50           55           60
133 ggt atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gag ttc act 240
134 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
135   65           70           75           80

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139      85      90      95
141 cag cag tat aat aac tgg cct ccg tac act ttt ggc cag ggg acc aag 336
142 Gln Gln Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys
143      100      105      110
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159 Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
160 20 25 30
162 Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro
163 35 40 45
165 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
166 50 55 60
168 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
169 65 70 75 80
171 Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
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187 <221> NAME/KEY: CDS
188 <222> LOCATION: (1)..(354)
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193 1 5 10 15
195 tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc agc agc tat 96
196 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
197 20 25 30
199 gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
200 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
201 35 40 45
203 gga ggg atc atc cct atc ttt ggt aca gca aac tac gca cag aag ttc 192
204 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe

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205      50      55      60
207 cag ggc aga gtc acg att acc gcg gac gaa tcc acg agc aca gcc tac 240
208 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
209 65      70      75      80
211 atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt 288
212 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
213      85      90      95
215 gcg aga gaa gat agc agt ggc tgg tat cac tac tgg ggc cag gga acc 336
216 Ala Arg Glu Asp Ser Ser Gly Trp Tyr His Tyr Trp Gly Gln Gly Thr
217      100      105      110
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220 Leu Val Thr Val Ser Ser
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233 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
234      20      25      30
236 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
237      35      40      45
239 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
240      50      55      60
242 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
243 65      70      75      80
245 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
246      85      90      95
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258 <213> ORGANISM: Homo sapiens
260 <220> FEATURE:
261 <221> NAME/KEY: CDS
262 <222> LOCATION: (1)..(333)
264 <400> SEQUENCE: 7
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267 1      5      10      15
269 aca gtc agg atc aca tgc caa gga gac agc ctc aga agc tat tat gca 96
270 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
271      20      25      30
273 agc tgg tac cag cag aag cca gga cag gcc cct gta ctt gtc atc tat 144

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274 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
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278 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
279          50          55          60
281 agc tca gga aac aca gct tcc ttg acc atc act ggg gct cag gcg gaa 240
282 Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
283 65          70          75          80
285 gat gag gct gac tat tac tgt aac tcc cgg gac agc agt ggt aac ccc 288
286 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn Pro
287          85          90          95
289 gtg gta ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag ccc 333
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306 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
307          35          40          45
309 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
310          50          55          60
312 Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
313 65          70          75          80
315 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn Pro
316          85          90          95
318 Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
319          100          105          110

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VERIFICATION SUMMARY

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